CLAIMS

1. A set of nucleic amplification primers capable of amplifying a VH-JH *IGH* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the VH family primers shown in Fig. 3B, or a variant thereof, and wherein said reverse primer is the JH consensus primer shown in Fig. 3B, or a variant thereof.

2. A set of nucleic amplification primers capable of amplifying a DH-JH *IGH* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the DH family primers shown in Fig. 4A, or a variant thereof, and wherein said reverse primer is the JH consensus primer shown in Fig. 4A, or a variant thereof.

3. A set of nucleic amplification primers capable of amplifying a VK-JK *IGK* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the VK family primers shown in Fig. 5B, or a variant thereof, and wherein said reverse primer is a JK primer shown in Fig. 5B, or a variant thereof.

4. A set of nucleic amplification primers capable of amplifying a VK/intron-Kde *IGK* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the VK primers or the INTR primer shown in Fig. 5B, or a variant thereof, and wherein said reverse primer is the Kde primer shown in Fig. 5B, or a variant thereof.

5. A set of nucleic amplification primers capable of amplifying a Vλ-Jλ *IGL* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Vλ primers shown in Fig. 6B, or a variant thereof, and wherein said reverse primer is the Jλ primer shown in Fig. 6B, or a variant thereof.

6. A set of nucleic amplification primers capable of amplifying a Vß-Jß *TCRB* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Vß family primers shown in Fig. 7B, or a variant thereof, and wherein said reverse primer is selected from the JßA en JβB primers shown in Fig. 7B, or a variant thereof.

7. A set of nucleic amplification primers capable of amplifying a Dß-Jß *TCRB* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Dß primers shown in Fig. 7B, or a variant thereof, and wherein said reverse primer is selected from the JßA en JßB primers shown in Fig. 7B, or a variant thereof.

8. A set of nucleic amplification primers capable of amplifying a Vγ-Jγ *TCRG* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Vγ family primers shown in Fig. 8B, or a variant thereof, and wherein said reverse primer is selected from the Jγ primers shown in Fig. 8B, or a variant thereof.

9. A set of nucleic amplification primers capable of amplifying a Vδ-Jδ *TCRD* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Vδ primers shown in Fig. 9B, or a variant thereof, and wherein said reverse primer is selected from the Jδ primers shown in Fig. 9B, or a variant thereof.

10. A set of nucleic amplification primers capable of amplifying a Dδ-Dδ *TCRD* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is the Dδ2 primer shown in Fig. 9B, or a variant thereof, and wherein said reverse primer is the Dδ3 primer shown in Fig. 9B, or a variant thereof.

11. A set of nucleic amplification primers capable of amplifying a Dδ-Jδ *TCRD* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is the Dδ2 primer shown in Fig. 9B, or a variant thereof, and wherein said reverse primer is selected from the Jδ primers shown in Fig. 9B, or a variant thereof.

12. A set of nucleic amplification primers capable of amplifying a Vδ-Dδ *TCRD* rearrangement comprising a forward primer and a reverse primer, wherein said forward primer is selected from the Vδ primers shown in Fig. 9B, or a variant thereof, and wherein said reverse primer is the Dδ3 primer shown in Fig. 9B, or a variant thereof.

13. A set of nucleic amplification primers capable of amplifying a chromosomal translocation (11;14)(*BCL1-IGH*) comprising a forward primer and a reverse primer, wherein said forward primer is the BCL1/MTC primer as shown in Fig. 10A, or a variant thereof, and wherein said reverse primer is the JH consensus primer shown in Fig. 10A, or a variant thereof.

14. A set of nucleic amplification primers capable of amplifying a chromosomal translocation t(14;18)(*BCL2-IGH*), comprising a forward primer and a reverse primer, wherein said forward primer is selected from the MBR primers, the 3'MBR primers and the mcr primers shown in Fig. 11A, or a variant thereof, and wherein said reverse primer is the JH consensus primer shown in Fig. 11A, or a variant thereof.

15. A set of nucleic amplification primers capable of amplifying the human *TBXAS1* gene comprising a forward and a reverse primer, wherein said forward primer is the

TBXAS1/X9U primer of Fig. 12 A, or a variant thereof, and wherein said reverse primer is the TBXAS1/X9L primer of Fig. 12A, or a variant thereof.

16. A set of nucleic amplification primers capable of amplifying the human recombination activating protein (*RAG1*) gene comprising a forward and a reverse primer, wherein said forward primer is the RAG1/X2U primer of Fig. 12A, or a variant thereof, and wherein said reverse primer is the RAG1/X2L primer of Fig. 12A, or a variant thereof.

17. A set of nucleic amplification primers capable of amplifying human promyelocytic leukemia zinc finger protein (*PLZF*) comprising a forward and a reverse primer, wherein said forward primer is the PLZF/X1U primer of Fig. 12A, or a variant thereof, and wherein said reverse primer is the PLZF/X1L primer of Fig. 12A, or a variant thereof.

18. A set of nucleic amplification primers capable of amplifying gene the human *AF4* gene (Exon 3) comprising a forward and a reverse primer, wherein said forward primer is the AF4/X3U primer of Fig. 12A, or a variant thereof, and wherein said reverse primer is the AF4/X3L primer of Fig. 12A, or a variant thereof.

19. A set of nucleic amplification primers capable of amplifying gene the human *AF4* gene (Exon11) comprising a forward and a reverse primer, wherein said forward primer is the AF4/X11U primer of Fig. 12A, or a variant thereof, and wherein said reverse primer is the AF4/X11L primer of Fig. 12A, or a variant thereof.

20. A nucleic acid amplification assay, preferably a PCR assay, more preferably a multiplex PCR assay, using at least one set of primers according to any one of claims 1 to 19.

21. A method for detecting a V_H-J_H *IGH* rearrangement, comprising using one or more sets of primers according to claim 1 in a nucleic acid amplification assay according to claim 20.

22. A method for detecting a D_H-J_H *IGH* rearrangement, comprising using one or more sets of primers according to claim 2 in a nucleic acid amplification assay according to claim 20.

23. A method for detecting a V_K-J_K *IGK* rearrangement, comprising using one or more sets of primers according to claim 3 in a nucleic acid amplification assay according to claim 20.

24. A method for detecting a V_K/intron-Kde IGK rearrangement, comprising using one or more sets of primers according to claim 4 in a nucleic acid amplification assay according to claim 20.

25. A method for detecting a Vλ-Jλ IGL rearrangement, comprising using one or more sets of primers according to claim 5 in a nucleic acid amplification assay according to claim 20.

26. A method for detecting a Vδ-Jδ TCRB rearrangement, comprising using one or more sets of primers according to claim 6 in a nucleic acid amplification assay according to claim 20.

27. A method for detecting a Dδ-Jδ TCRB rearrangement, comprising using one or more sets of primers according to claim 7 in a nucleic acid amplification assay according to claim 20.

28. A method for detecting a Vγ-Jγ TCRG rearrangement, comprising using one or more sets of primers according to claim 8 in a nucleic acid amplification assay according to claim 20.

29. A method for detecting a Vδ-Jδ TCRD rearrangement, comprising using one or more sets of primers according to claim 9 in a nucleic acid amplification assay according to claim 20.

30. A method for detecting a Dδ-Dδ TCRD rearrangement, comprising using one or more sets of primers according to claim 10 in a nucleic acid amplification assay according to claim 20.

31. A method for detecting a Dδ-Jδ TCRD rearrangement, comprising using one or more sets of primers according to claim 11 in a nucleic acid amplification assay according to claim 20.

32. A method for detecting a Vδ-Dδ TCRD rearrangement, comprising using one or more sets of primers according to claim 12 in a nucleic acid amplification assay according to claim 20.

33. A method for detecting a chromosomal translocation (11;14)(*BCL1-IGH*), comprising using one or more sets of primers according to claim 13 in a nucleic acid amplification assay according to claim 20.

34. A method for detecting a chromosomal translocation t(14;18)(BCL2-IGH), comprising using one or more sets of primers according to claim 14 in a nucleic acid amplification assay according to claim 20.

35. A method for detecting a gene selected from the group consisting of the human *AF4* gene (exon 3), the human *AF4* gene (exon 11), the human *PLZF1* gene, the human *RAG1* gene and the human *TBXAS1* gene, comprising using one or more sets of primers according to any one of claims 15 to 19 in a nucleic acid amplification assay according to claim 20.

36. Use of a method according to claim 35 to assess the quality of a DNA sample extracted from a biological sample, preferably a paraffin-embedded biological sample.

37. A method for detecting two or more rearrangements, two or more translocations or at least one rearrangement and at least one translocation selected from the group consisting of a V_H-J_H *IGH* rearrangement, a D_H-J_H *IGH* rearrangement, a V_K-J_K *IGK* rearrangement, a V_K/intron-Kde *IGK* rearrangement, a Vλ-Jλ IGL rearrangement, a Vβ-Jβ *TCRB* rearrangement, a Dβ-Jβ *TCRB* rearrangement, a V_γ-J_γ *TCRG* rearrangement, a Vδ-Jδ *TCRD* rearrangement, a Dδ-Dδ *TCRD* rearrangement, a Dδ-Jδ *TCRD* rearrangement, a Vδ-Dδ *TCRD* rearrangement, a t(11;14)(*BCL1-IGH*) translocation and t(14;18)(*BCL2-IGH*) translocation, using at least two sets of primers according to any one of claims 1 or 14.

38. A method for assessing clonal rearrangements and/or chromosome aberrations using at least one set of primers according to any one of claims 1 to 14, and optionally at least one set of primers according to any one of claims 15 to 19.

39. A method according to claim 38 for the detection of minimal residual disease (MRD) or for identification of PCR targets to be used for MRD detection via real-time quantitative PCR.

40. A method according to claim 38 or 39, wherein an amplified nucleic acid is detected using automated high resolution PCR fragment analysis.

41. A kit for the detection of at least one rearrangement selected from the group consisting of a V_H-J_H *IGH* rearrangement, a D_H-J_H *IGH* rearrangement, a V_K-J_K *IGK* rearrangement, a V_K/intron-Kde *IGK* rearrangement, a Vλ-Jλ *IGL* rearrangement, a Vβ-Jβ *TCRB* rearrangement, a Dβ-Jβ *TCRB* rearrangement, a V_γ-J_γ *TCRG* rearrangement, a Vδ-Jδ *TCRD* rearrangement, a Dδ-Dδ *TCRD* rearrangement, a Dδ-Jδ *TCRD* rearrangement, a Vδ-Dδ *TCRD*, and/or at least one translocation selected from t(11;14)(*BCL1-IGH*) and t(14;18)(*BCL2-IGH*), comprising at least one set of primers according to any one of claims 1 to 14.

42. A kit according to claim 41, further comprising at least one set of primers according to any one of claims 15 to 19.